#19

1646

```
      RAW SEQUENCE LISTING              DATE: 02/20/2001
      PATENT APPLICATION: US/09/114,844B    TIME: 16:25:58

         Input Set : A:\P1129R1 (REVISED).txt
         Output Set: N:\CRF3\02202001\I114844B.raw

 3  <110> APPLICANT: Ashkenazi, Avi J.
 4         Gurney, Austin
 6  <120> TITLE OF INVENTION: RTD Receptor
 8  <130> FILE REFERENCE: P1129R1 (REVISED)
10  <140> CURRENT APPLICATION NUMBER: US 09/114,844B
11  <141> CURRENT FILING DATE: 1998-07-14
13  <150> PRIOR APPLICATION NUMBER: US 60/056,974
14  <151> PRIOR FILING DATE: 1997-08-26
16  <160> NUMBER OF SEQ ID NOS: 10
18  <210> SEQ ID NO: 1
19  <211> LENGTH: 386
20  <212> TYPE: PRT
21  <213> ORGANISM: Homo sapiens
23  <220> FEATURE:
24  <221> NAME/KEY: unsure
25  <222> LOCATION: 310
26  <223> OTHER INFORMATION: Xaa may be serine or leucine
28  <400> SEQUENCE: 1
29  Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
30    1           5                  10                  15
32  Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
33                 20                  25                  30
35  Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
36                 35                  40                  45
38  Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
39                 50                  55                  60
41  Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
42                 65                  70                  75
44  Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
45                 80                  85                  90
47  Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
48                 95                  100                 105
50  Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
51                 110                 115                 120
53  Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
54                 125                 130                 135
56  Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
57                 140                 145                 150
59  Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
60                 155                 160                 165
62  Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
63                 170                 175                 180
65  Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
66                 185                 190                 195
68  Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
69                 200                 205                 210
71  His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val
```

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Input Set : A:\P1129R1 (REVISED).txt
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```
 72                    215                 220                 225
 74   Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
 75                    230                 235                 240
 77   Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
 78                    245                 250                 255
 80   Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
 81                    260                 265                 270
 83   Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
 84                    275                 280                 285
 86   Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
 87                    290                 295                 300
 89   Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
 90                    305                 310                 315
 92   Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
 93                    320                 325                 330
 95   Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
 96                    335                 340                 345
 98   Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
 99                    350                 355                 360
101    Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
102                    365                 370                 375
104    Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
105                    380                 385
107   <210> SEQ ID NO: 2
108   <211> LENGTH: 2082
109   <212> TYPE: DNA
110   <213> ORGANISM: Homo sapiens
112   <220> FEATURE:
113   <221> NAME/KEY: unsure
114   <222> LOCATION: 1085
115   <223> OTHER INFORMATION: Y may be cytosine, thymine or uracil
117   <400> SEQUENCE: 2
118   ccaactgcac ctcggttcta tcgattgaat tccccgggga tcctctagag 50
120   atccctcgac ctcgacccac gcgtccggaa cctttgcacg cgcacaaact 100
122   acggggacga tttctgattg atttttggcg ctttcgatcc accctcctcc 150
124   cttctc atg gga ctt tgg gga caa agc gtc ccg acc gcc 189
125          Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
126            1               5                  10
128   tcg agc gct cga gca ggg cgc tat cca gga gcc agg aca 228
129   Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
130             15                  20
132   gcg tcg gga acc aga cca tgg ctc ctg gac ccc aag atc 267
133   Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
134   25                  30                  35
136   ctt aag ttc gtc gtc ttc atc gtc gcg gtt ctg ctg ccg 306
137   Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
138          40                  45                  50
140   gtc cgg gtt gac tct gcc acc atc ccc cgg cag gac gaa 345
141   Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu
```

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PATENT APPLICATION:  US/09/114,844B     TIME: 16:25:58

Input Set : A:\P1129R1 (REVISED).txt
Output Set: N:\CRF3\02202001\I114844B.raw

```
142                    55                    60
144   gtt ccc cag cag aca gtg gcc cca cag caa cag agg cgc 384
145   Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
146         65                    70                    75
148   agc ctc aag gag gag gag tgt cca gca gga tct cat aga 423
149   Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
150               80                    85
152   tca gaa tat act gga gcc tgt aac ccg tgc aca gag ggt 462
153   Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
154   90                    95                   100
156   gtg gat tac acc att gct tcc aac aat ttg cct tct tgc 501
157   Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys
158         105                   110                   115
160   ctg cta tgt aca gtt tgt aaa tca ggt caa aca aat aaa 540
161   Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys
162               120                   125
164   agt tcc tgt acc acg acc aga gac acc gtg tgt cag tgt 579
165   Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys
166         130                   135                   140
168   gaa aaa gga agc ttc cag gat aaa aac tcc cct gag atg 618
169   Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met
170               145                   150
172   tgc cgg acg tgt aga aca ggg tgt ccc aga ggg atg gtc 657
173   Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val
174   155                   160                   165
176   aag gtc agt aat tgt acg ccc cgg agt gac atc aag tgc 696
177   Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
178         170                   175                   180
180   aaa aat gaa tca gct gcc agt tcc act ggg aaa acc cca 735
181   Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro
182               185                   190
184   gca gcg gag gag aca gtg acc acc atc ctg ggg atg ctt 774
185   Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu
186         195                   200                   205
188   gcc tct ccc tat cac tac ctt atc atc ata gtg gtt tta 813
189   Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu
190               210                   215
192   gtc atc att tta gct gtg gtt gtg gtt ggc ttt tca tgt 852
193   Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys
194   220                   225                   230
196   cgg aag aaa ttc att tct tac ctc aaa ggc atc tgc tca 891
197   Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser
198         235                   240                   245
200   ggt ggt gga gga ggt ccc gaa cgt gtg cac aga gtc ctt 930
201   Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu
202               250                   255
204   ttc cgg cgg cgt tca tgt cct tca cga gtt cct ggg gcg 969
205   Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
206         260                   265                   270
```

```
208  gag gac aat gcc cgc aac gag acc ctg agt aac aga tac 1008
209  Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
210              275                 280
212  ttg cag ccc acc cag gtc tct gag cag gaa atc caa ggt 1047
213  Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
214  285                 290                 295
216  cag gag ctg gca gag cta aca ggt gtg act gta gag tyg 1086
217  Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
218              300                 305                 310
220  cca gag gag cca cag cgt ctg ctg gaa cag gca gaa gct 1125
221  Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
222              315                 320
224  gaa ggg tgt cag agg agg agg ctg ctg gtt cca gtg aat 1164
225  Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
226      325                 330                 335
228  gac gct gac tcc gct gac atc agc acc ttg ctg gat gcc 1203
229  Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
230              340                 345
232  tcg gca aca ctg gaa gaa gga cat gca aag gaa aca att 1242
233  Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
234  350                 355                 360
236  cag gac caa ctg gtg ggc tcc gaa aag ctc ttt tat gaa 1281
237  Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
238              365                 370                 375
240  gaa gat gag gca ggc tct gct acg tcc tgc ctg tgaaag 1320
241  Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
242              380                 385
244  aatctcttca ggaaaccaga gcttccctca tttacctttt ctcctacaaa 1370
246  gggaagcagc ctggaagaaa cagtccagta cttgacccat gccccaacaa 1420
248  actctactat ccaatatggg gcagcttacc aatggtccta gaactttgtt 1470
250  aacgcacttg gagtaatttt tatgaaatac tgcgtgtgat aagcaaacgg 1520
252  gagaaattta tatcagattc ttggctgcat agttatacga ttgtgtatta 1570
254  agggtcgttt taggccacat gcggtggctc atgcctgtaa tcccagcact 1620
256  ttgataggct gaggcaggtg gattgcttga gctcgggagt ttgagaccag 1670
258  cctcatcaac acagtgaaac tccatctcaa tttaaaaaga aaaaaagtgg 1720
260  ttttaggatg tcattctttg cagttcttca tcatgagaca agtctttttt 1770
262  tctgcttctt atattgcaag ctccatctct actggtgtgt gcatttaatg 1820
264  acatctaact acagatgccg cacagccaca atgctttgcc ttatagtttt 1870
266  ttaactttag aacgggatta tcttgttatt acctgtattt tcagtttcgg 1920
268  atattttgat cttaatgatg agattatcaa gacgtacccc tatgctaagt 1970
270  catgagcata tggacttacg agggttcgac ttagagtttt gagctttaag 2020
272  ataggattat tgggggctta cccccacctt aattagaaga aacattttat 2070
274  attgctttac ta 2082
276  <210> SEQ ID NO: 3
277  <211> LENGTH: 50
278  <212> TYPE: DNA
279  <213> ORGANISM: Artificial sequence
281  <220> FEATURE:
282  <223> OTHER INFORMATION: Sequence is synthesized.
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RAW SEQUENCE LISTING
PATENT APPLICATION:  US/09/114,844B

DATE: 02/20/2001
TIME: 16:25:58

Input Set : A:\P1129R1 (REVISED).txt
Output Set: N:\CRF3\02202001\I114844B.raw

```
284 <400> SEQUENCE: 3
285  cataaaagtt cctgcaccat gaccagagac acagtgtgtc agtgtaaaga 50
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 24
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Sequence is synthesized.
295 <400> SEQUENCE: 4
296  cttcaggaaa ccagagcttc cctc 24
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 24
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Sequence is synthesized.
306 <400> SEQUENCE: 5
307  ttctcccgtt tgcttatcac acgc 24
309 <210> SEQ ID NO: 6
310 <211> LENGTH: 191
311 <212> TYPE: PRT
312 <213> ORGANISM: Homo sapiens
314 <400> SEQUENCE: 6
315  Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro Ser
316    1               5                  10                  15
318  Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg
319                  20                  25                  30
321  Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val
322                  35                  40                  45
324  Val Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr
325                  50                  55                  60
327  Ile Lys Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His
328                  65                  70                  75
330  Ser Pro Leu Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu
331                  80                  85                  90
333  Arg Pro Gly Ala Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr
334                  95                  100                 105
336  Asn Ala Ser Asn Asn Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys
337                  110                 115                 120
339  Lys Ser Asp Glu Glu Glu Arg Ser Pro Cys Thr Thr Thr Arg Asn
340                  125                 130                 135
342  Thr Ala Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser
343                  140                 145                 150
345  Ala Glu Met Cys Arg Lys Cys Ser Thr Gly Cys Pro Arg Gly Met
346                  155                 160                 165
348  Val Lys Val Lys Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val
349                  170                 175                 180
351  His Lys Glu Ser Gly Asn Gly His Asn Ile Trp
352                  185                 190
```

VERIFICATION SUMMARY
PATENT APPLICATION:  US/09/114,844B

DATE: 02/20/2001
TIME: 16:25:59

Input Set : A:\P1129R1 (REVISED).txt
Output Set: N:\CRF3\02202001\I114844B.raw

L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2